Fig. 1

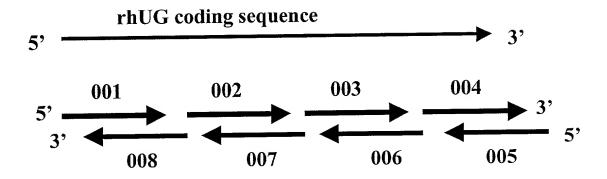


Fig. 2

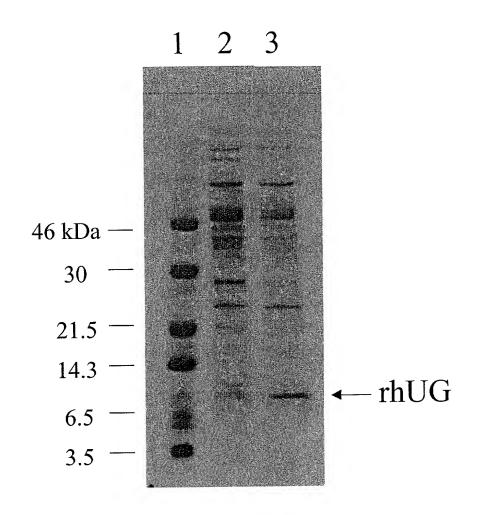


Fig. 3

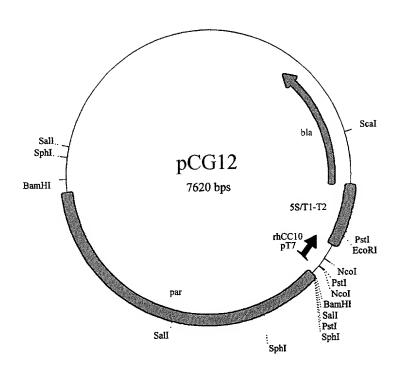


Fig. 4

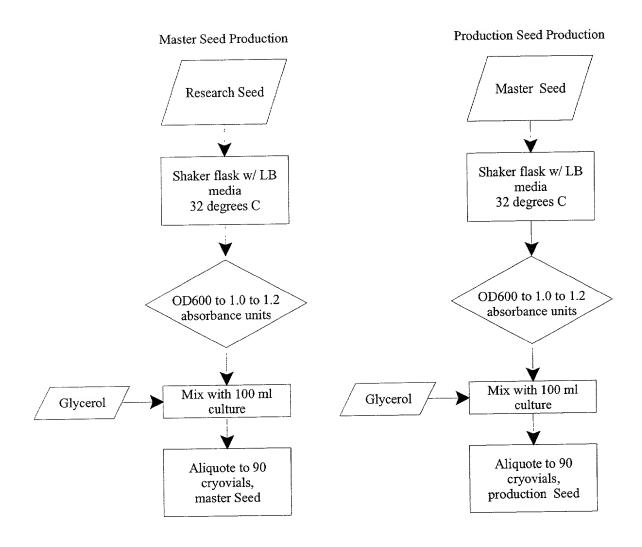


Fig. 5

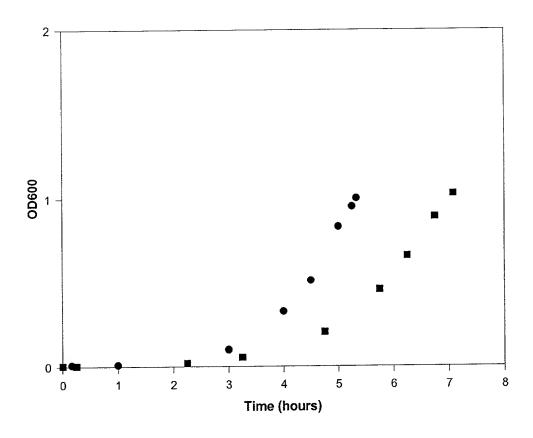


Fig. 6

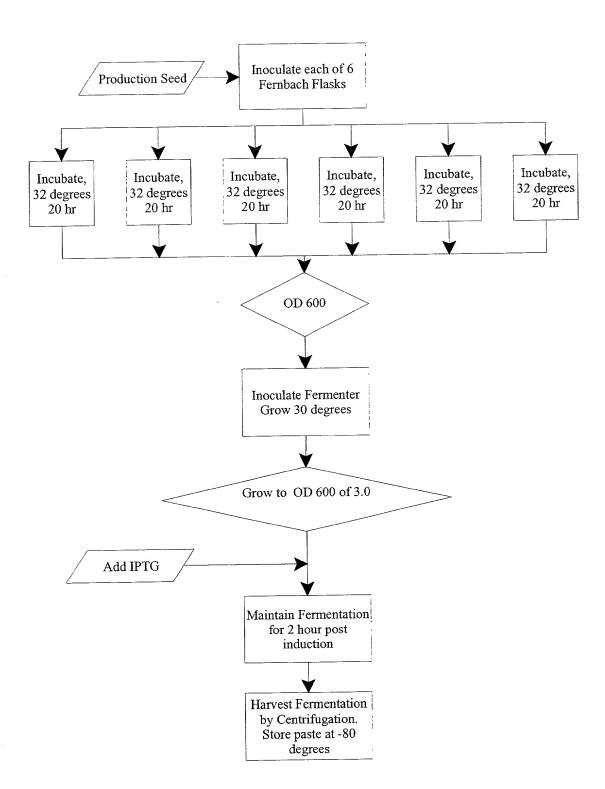


Fig. 7

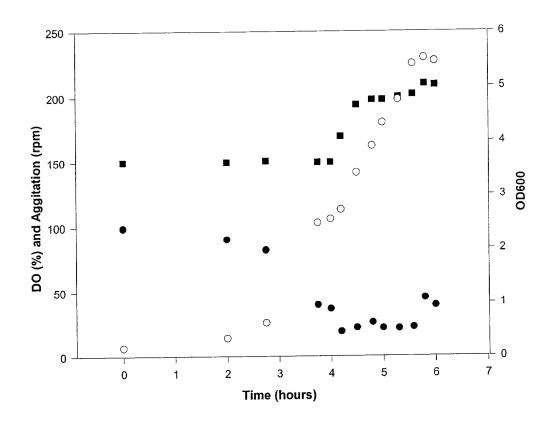


Fig. 8

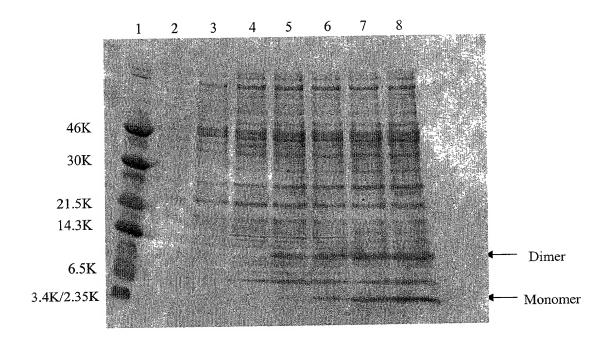


Fig. 9a

Purification used in Initial Toxicology study

Cell Lysis by Shear



Tangential Flow Filtration,
Polyethersulfone Membrane (100,000
NMWCO)



Tangential Flow Filtration,
Concentration
Polyethersulfone Membrane (5,000
NMWCO)



Anion Exchange Chromatography, Elution with Sodium Chloride

Tangential Flow Filtration, Concentration/Buffer exchange Polyethersulfone Membrane (5,000 NMWCO)



Type I, Hydroxyapatite, Elution with Sodium Phosphate



Tangential Flow Filtration, Polyethersulfone Membrane (30,000 NMWCO)



Tangential Flow Filtration, Concentration/Buffer Exchange Polyethersulfone Membrane (5,000 NMWCO)

Fig. 9b

Purification used in first cGMP Manufacturing Run

Cell Lysis by Shear



Tangential Flow Filtration, Polyethersulfone Membrane (100,000 NMWCO)



Tangential Flow Filtration, Concentration /Diafiltration Polyethersulfone Membrane (5,000 NMWCO)



Anion Exchange Chromatography, Elution with Sodium Chloride



Tangential Flow Filtration, Concentration/Buffer exchange Polyethersulfone Membrane (5,000 NMWCO)



Type I, Hydroxyapatite, Elution with Sodium Phosphate



Copper Immobilized Metal Affinity Chromatography



Filtration through SartoBind Q Anion Exchange Membrane



Tangential Flow Filtration, Concentration/Buffer Exchange Polyethersulfone Membrane (5,000 NMWCO)

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Fig. 10

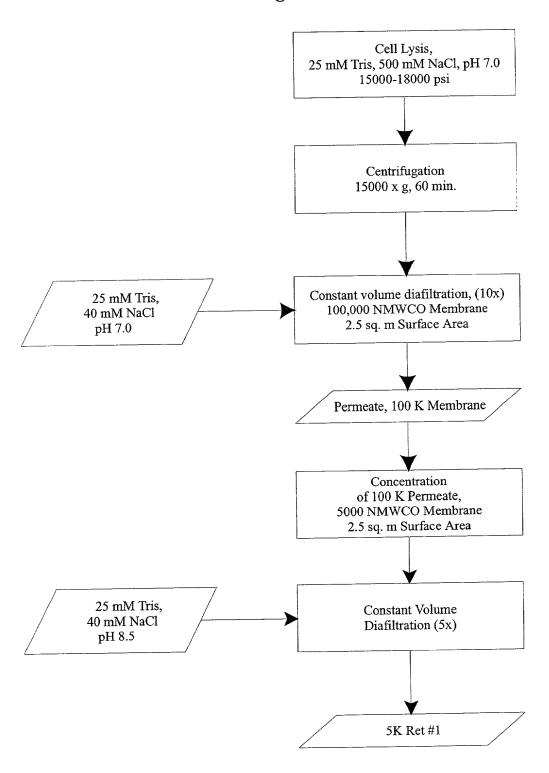


Fig. 11a

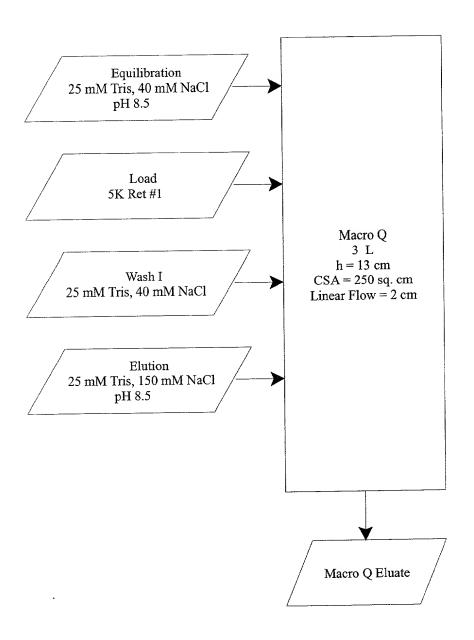


Fig. 11b

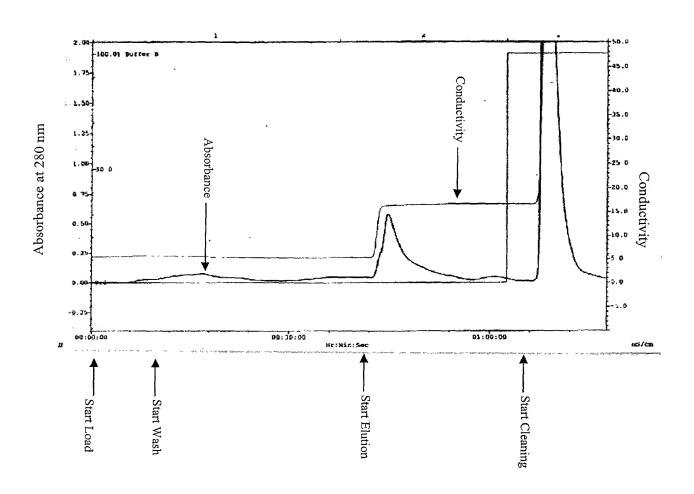


Fig. 12

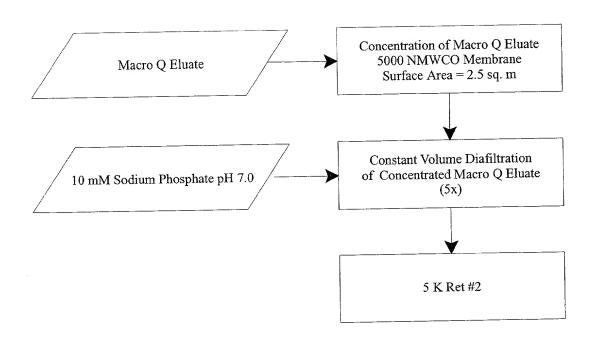


Fig. 13a

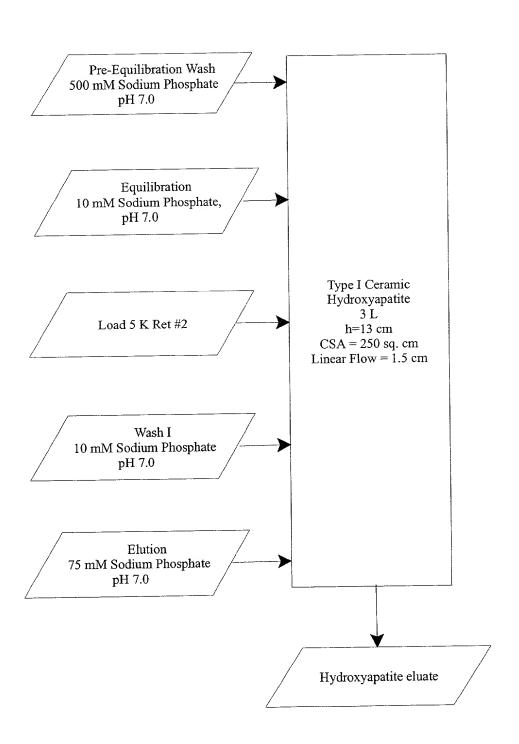


Fig. 13b

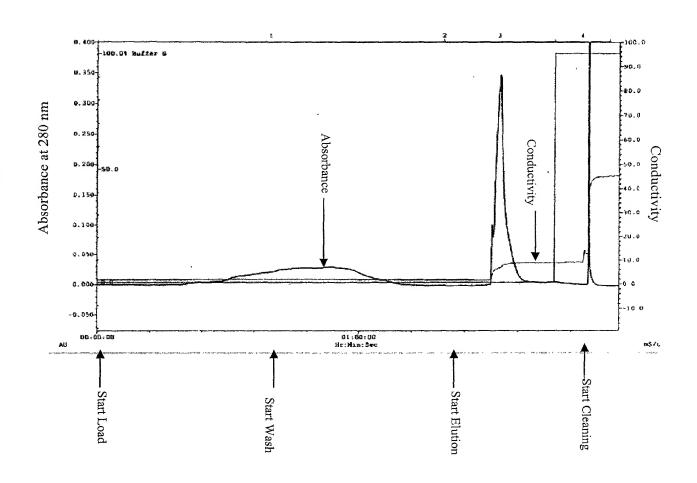


Fig. 14a

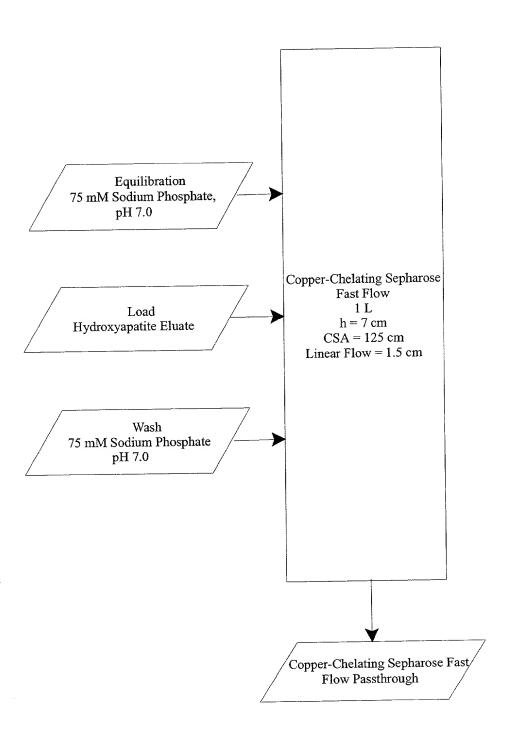


Fig. 14b

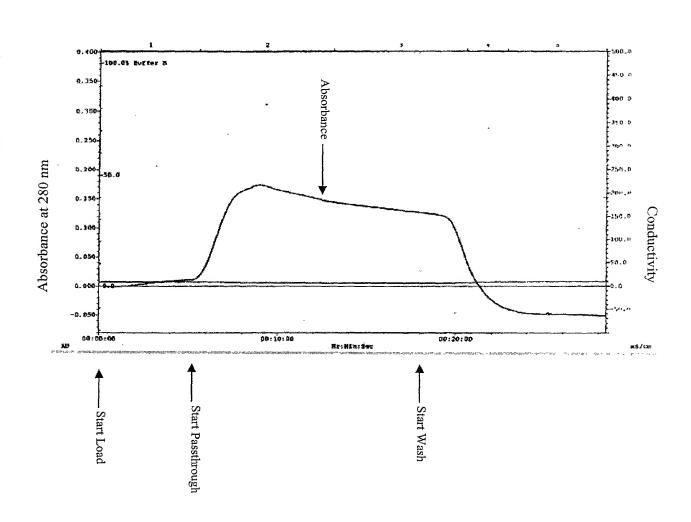
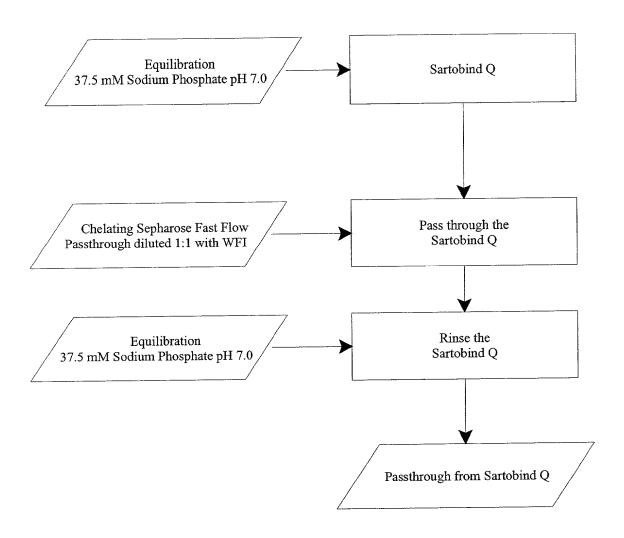


Fig. 15



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Fig. 16

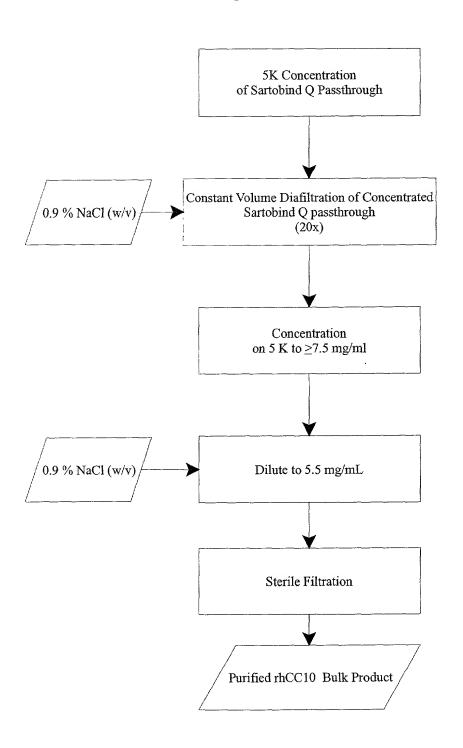
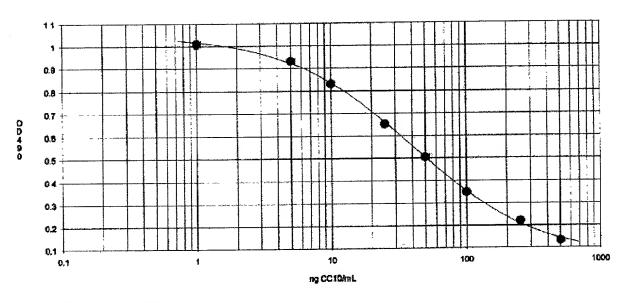


Fig. 17



4 Parameters y = (a-d)/(1+(x/c)*b) + d a=1.047 b=0.9322 c=40.73 d=0.05497 R=0.9997 R=0.9994 brr=0.007895

Fig. 18

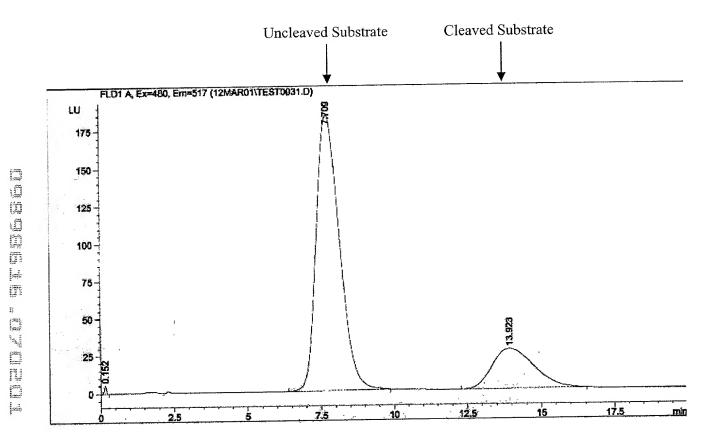


Fig. 19

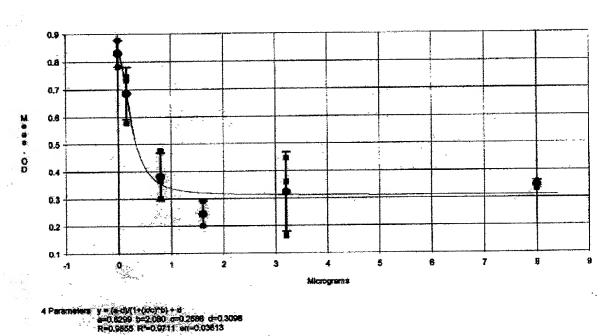


Fig. 20a

1 2 3 4 5 6 7 8 9

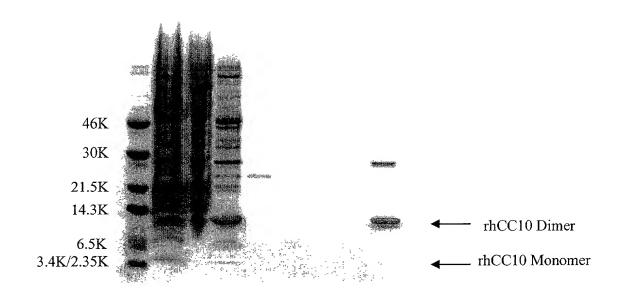


Fig. 20b

1 2 3 4 5 6 7

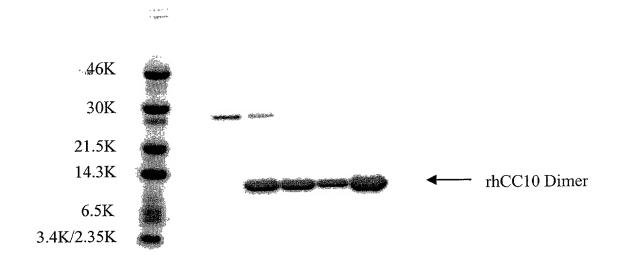
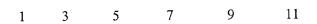


Fig. 21



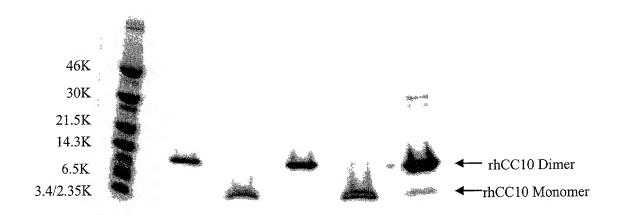


Fig. 22

1 2 3 4 5 6

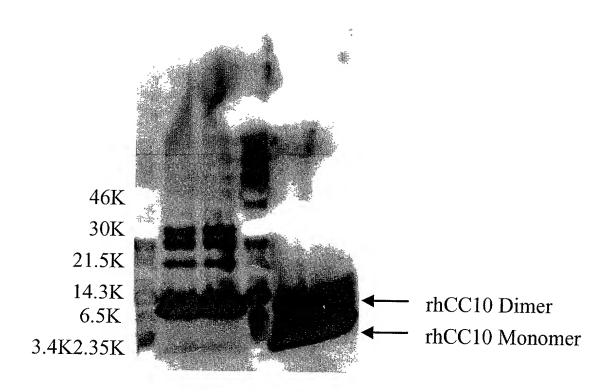


Fig. 23

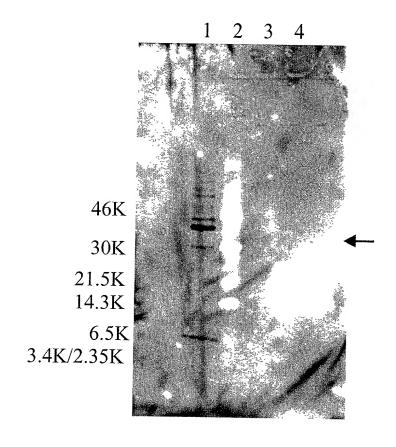
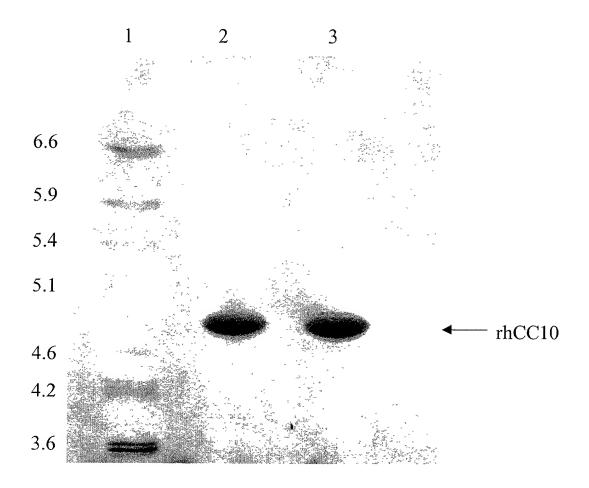
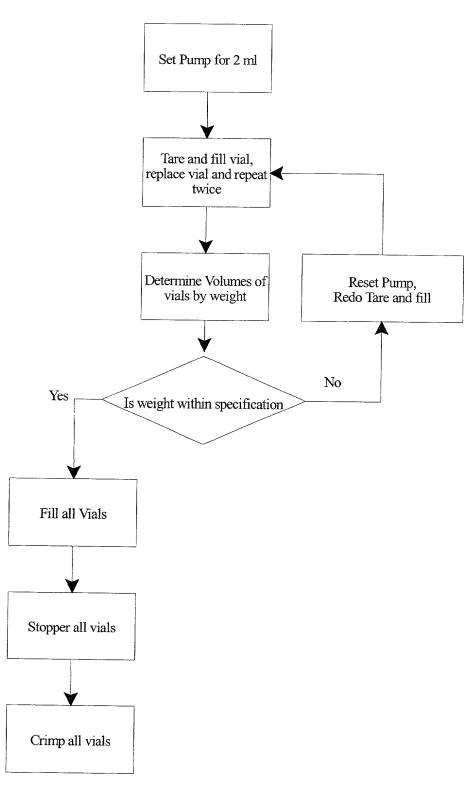


Fig. 24



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Fig. 25



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Fig. 26

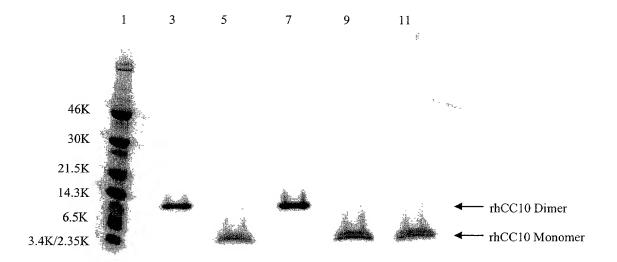


Fig. 27

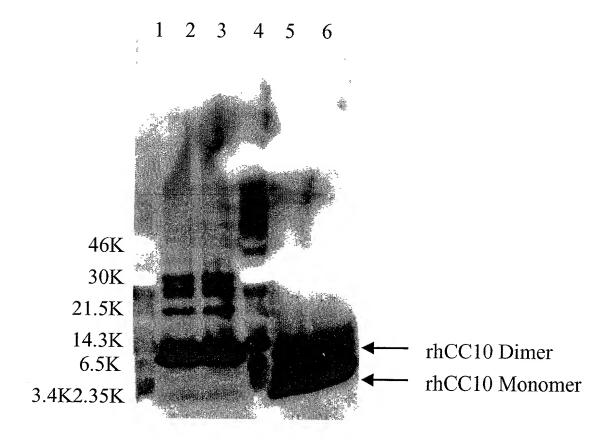


Fig. 28

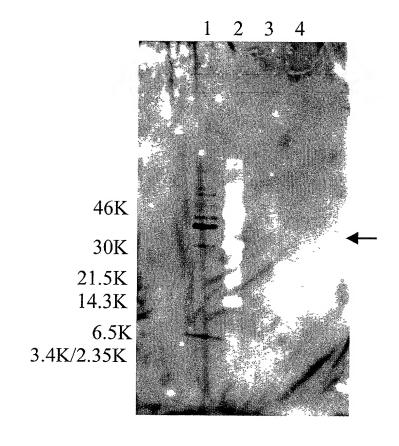


Fig. 29

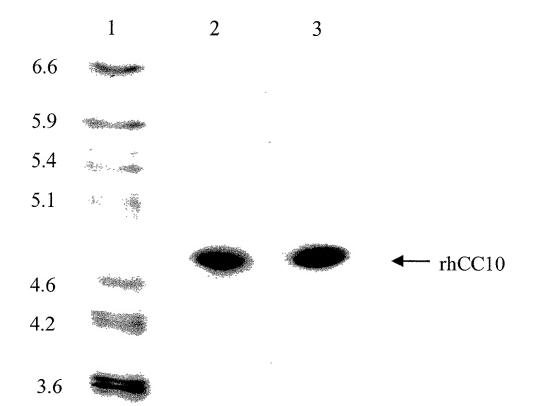


Fig. 30

TATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTC GGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCC AGCAAAAGGCCAGGAACCGTAAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCA GAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGAT ACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCT GTGTGCACGAACCCCCGGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCA GCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACCGGCTACACTAGAAGGACA TTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACT GAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTC GTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAA TGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCAT TCTGAGAATAGTGTATGCGGGGGACCGAGTTGCTCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATT GGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATC TTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCAT ACTGAGCCTTCGATTCATTCATGCCTGGCAGTTCCCTACTCTCGCATGGGGAGACCCCACACTACCATCGGCGCTACGGCGTTTCACTTCTGAGTTC
GGCATGGGGTCAGGTGGGACCACCGCGCTACTGCCGCCAGGCAAATTCTGTTTTATCAGACCGCTTCTGCGTTCTGATTTAATCTGTATCAGGCTGAA TCAGGGCTGAAAAGTTCCATGGCAGCCTCATAACTGGAGGGTGTGTCCATGAGGAGGGTTTCGATGACACGCTGAAAGCTCGGGCAGATCTCTGCAGCCATGGTGTATAATCTCCTTCTTAAAGTTAACAAAAATTATTTCTAGAGGGAAAACCGTTGTGGTCTCCCTATAGTGAGTCGTATTAATTTGGATCCTCTAG GGCGTTCCTCGGCGAACATAGCGGCATGGTGGCCTTCGGCTTCTTCCGCGACCAGGTGAAGGACATGCACTGCGATGCGGACGTGATCCTGGCCCGG A CACCGAGGGGAAAAGCGAGGATCTAGGTAGGGCGCTCGCAGCGGCCCTGCGGGACGCGAAAAGGTGAGAAAAGCCGGGCACTGCCCGGCTTTATTTTTGCTGCTGCGCGTTCCAGGCCGCCCACACTCGTTTGACCTGGCTCGGGCTGCATCCGACCAGCTTGGCCGTCTTGGCAATGCTCGATCCGCCGGAG GCAAGCGGCTGATGCGGTCGATCTTCTCCGCAACGACGACTTCACCAGGTTGCAGGTCCGCGATCATGCGCAGCAGCTCGGGCCGGTCGGCGCGTGC TACTGGCGCGCAGGTAGATGCGGGCGACCTTCAACCTTCGTCCCTCCGGTTGTTGCTCTCGCGTCGCCATTTCCACGGCTCGACGGCGTGCGGATCGG ACCAGAGGCCGACGCGTTGCCTCGCGCCTCCTGTTCGAGCCGCAGCATTTCAGGGTCGGCCGCGGCGCGTGGAAGCGATAGGCCCACGCCATGCC GTCAATGTCCACCAGGCGCACGCGCACCGGCTGCTTGTCTACCAGCACGTCGATGGTGTCGCCGTCGATGATGCGCACGACCTCGCCGCGCAGCTCG TCCTCACGGCTGAGGCCGAAGCCGATCTACGCGGCATCATCCGCTACACGCGCCGGGAGTGGGGCGCGGCGCAGGTGCGCCGCTATATCGCTAAGCT GGAACAGGGCATAGCCAGGCTTACGCGGCAAGGCCCGTTTAAGGACATGAGCGAACTCTTTCCCGCGCTGCGATGGCCCGCTGCGAACACCAC TACGTTTTTTGCCTGCCGCGTGCGGGCGAACCCGCGTTGGTCGTCGTCGCGATCCTGCATGAGCGCATGGACCTCATGACGCGACTTGCCGACAGGCTCAA GGGCTGATTTCAGCCGCTAAAAAATCGCGCCACTCACAACGTCCTGATGGCGTACTTACCCAAAGAACAGCTAGGAGAATCATTTATGCTCAGCACACTTCCACAAAGCTCATGCAACTTTCTTGAACCGCATCCGCGATGCGGTCGCTTCCGATGTTCGCTTCCGCGCTCTTCTGATCGGCGGCTCTTACGTTCACG GAGGACTCGATGAGCACTTCGATTTGGACATCGTTGTTGAGGACAACTGCTACGCAGATGTCTTGTCTACACGCAAGGATTTTGCCGAGGCA CTGCCCGGCTTCCTCAACGCGATAAGCTGGCTGGATCCTCTACGCCGGACGCATCGTGGCCGGCACACGCGCGCACAGGTGCGGTTGCTGGCGCCCT $CGCATAAGGGAGAGCGTCGACCGATGCCCTTGAGAGCCTTCAACCCAGTCAGCTCCTTCCGGTGGGCGCGGGGCATGACTATCGTCGCCGCACTTAT\\GACTGTCTTCTTTATCATGCAACTCGTAGGACAGGTGCCGGCAGCGCTCTGGGTCATTTTCGGCGAGGACCGCTTTCGCTGGAGCGCGACGATGATCG\\$ GCCTGTCGCTTGCGGTATTCGGAATCTTGCACGCCCTCGCTCAAGCCTTCGTCACTGGTCCCGCCACCAAACGTTTCGGCGAGAAGCAGGCCATTATC GCCGGCATGGCGGCCGACGCGCTGGGCTACGTCTTGCTGGCGTTCGCGACGCGAGGCTGGATGGCCTTCCCCATTATGATTCTTCTCGCTTCCGGCGG ACTTCGATCATTGGACCGCTGATCGTCACGGCGATTTATGCCGCCTCGGCGAGCACATGGAACGGGTTGGCATGGATTGTAGGCGCCCCCTATACCT TGTCTGCCTCCCGCGTTGCGTCGCGGTGCATGGAGCCGGGCCACCTCGACCTGAATGGAAGCCGGCGGCACCTCGCTAACGGATTCACCACTCCAA ${\sf GCGGCGCATCTCGGGCAGCGTTGGGTCCTGGCCACGGGTGCGCATGATCGTGCTCCTGTCGTTGAGGACCCGGCTAGGCTGGCGGGGTTGCCTTACTG}$ GTTAGCAGAATGAATCACCGATACGCGAGCGAACGTGAAGCGACTGCTGCTGCAAAACGTCTGCGACCTGAGCAACAACATGAATGGTCTTCGGTTT AGGCATCAGTGACCAAACAGGAAAAAACCGCCCTTAACATGGCCCGCTTTATCAGAAGCCAGACATTAACGCTTCTGGAGAAACTCAACGAGCTGGA CGCGGATGAACAGGCAGACATCTGTGAATCGCTTCACGACCACGCTGATGAGCTTTACCGCAGCTGCCTCGCGCGTTTCGGTGATGACGGTGAAAACGGTGTCGGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATACTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCAC

Fig. 31

Met Ala Ala Glu Ile Cys Pro Ser Phe Gln Arg Val Ile Glu Thr Leu Leu Met Asp Thr Pro Ser Ser Tyr Glu Ala Ala Met Glu Leu Phe Ser Pro Asp Gln Asp Met Arg Glu Ala Gly Ala Gln Leu Lys Lys Leu Val Asp Thr Leu Pro Gln Lys Pro Arg Glu Ser Ile Ile Lys Leu Met Glu Lys Ile Ala Gln Ser Ser Leu Cys Asn